

We claim:

1. The use of a polypeptide with the biological activity of an  
5 NADH-dependent cytochrome b5 reductase encoded by a nucleic  
acid sequence consisting of
  - a) a nucleic acid sequence with the nucleic acid sequence  
shown in SEQ ID NO:1; or  
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  - b) a nucleic acid sequence which, on the basis of the  
degeneracy of the genetic code, can be deduced from the  
amino acid sequence shown in SEQ ID NO:2 by back  
translation; or  
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  - c) a nucleic acid sequence which, on the basis of the  
degeneracy of the genetic code, can be deduced from the  
amino acid sequence of a functional equivalent of SEQ ID  
NO:2, which has at least 39% identity with SEQ ID NO:2,  
20 by back translation; or
  - d) a functional equivalent of the nucleic acid sequence SEQ  
ID NO:1 with at least 52% identity with SEQ ID NO:1,  
25 as target for herbicides.
2. A plant nucleic acid sequence encoding a polypeptide with the  
biological activity of an NADH-dependent cytochrome b5  
30 reductase comprising a part-region encompassing:
  - a) a nucleic acid sequence with the nucleic acid sequence  
shown in SEQ ID NO:3; or
  - 35 b) a nucleic acid sequence which, on the basis of the  
degeneracy of the genetic code, can be deduced from the  
amino acid sequence shown in SEQ ID NO:4 by back  
translation; or
  - 40 c) a functional equivalent of the nucleic acid sequence SEQ  
ID NO:3 with at least 77% identity with SEQ ID NO:3;
  - 45 d) a nucleic acid sequence which, on the basis of the  
degeneracy of the genetic code, can be deduced from the  
amino acid sequence of a functional equivalent of SEQ ID  
NO:4, which has at least 87% identity with SEQ ID NO:4,  
by back translation.

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3. A polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase as target for herbicides, encoded by a nucleic acid molecule as claimed in claim 2.  
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4. A method for detecting functional analogues of SEQ ID NO:1
  - a) by preparing a probe and subsequently screening a genomic library or a cDNA library of the species in question; or  
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  - b) by a computer search for analogous sequences in electronic databases.
5. An expression cassette comprising
  - a) genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 2; or  
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  - b) additional functional elements; or  
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  - c) a combination of a) and b).
6. A vector comprising an expression cassette as claimed in claim 5.  
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7. A nonhuman transgenic organism comprising at least one nucleic acid sequence encoding a polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase as claimed in claim 2, an expression cassette as  
30 claimed in claim 5 or a vector as claimed in claim 6 selected from among bacteria, yeasts, fungi, animal cells or plant cells.
8. The use of a polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase encoded by a nucleic acid sequence consisting of
  - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1; or  
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  - b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translation; or  
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- c) a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 52% identity with SEQ ID NO:1;
- d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence of a functional equivalent of SEQ ID NO:2, which has at least 39% identity with SEQ ID NO:2, by back translation,
- in a method for identifying herbicidally active compounds.
9. A method for identifying herbicidally active compounds, encompassing the following steps:
- i. bringing a polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase encoded by a nucleic acid sequence consisting of
- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1; or
- b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translation; or
- c) a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 52% identity with SEQ ID NO:1; or
- d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence of a functional equivalent of SEQ ID NO:2, which has at least 39% identity with SEQ ID NO:2, by back translation
- into contact with one or more test compounds under conditions which allow the test compound(s) to bind to the NADH-dependent cytochrome b5 reductase; and
- ii. detecting whether the test compound binds to the NADH-dependent cytochrome b5 reductase of i); or
- iii. detecting whether the test compound reduces or blocks the activity of the NADH-dependent cytochrome b5 reductase of i); or

- iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the NADH-dependent cytochrome b5 reductase of i).

5 10. A method as claimed in claim 9, which comprises

- i. either expressing, in a transgenic organism, NADH-dependent cytochrome b5 reductase which is encoded by a nucleic acid sequence consisting of

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- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1; or

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- b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translation; or

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- c) a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 52% identity with SEQ ID NO:1; or

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- d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence of a functional equivalent of SEQ ID NO:2, which has at least 39% identity with SEQ ID NO:2, by back translation

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or culturing an organism which naturally contains NADH-dependent cytochrome b5 reductase;

- ii. bringing the NADH-dependent cytochrome b5 reductase of step i) in a cell digest of the transgenic or nontransgenic organism, in partially or homogeneously purified form, into contact with a test compound; and

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- iii. selecting a test compound which reduces or blocks the activity of the NADH-dependent cytochrome b5 reductase of step i), where the activity of the NADH-dependent cytochrome b5 reductase incubated with the test compound is compared with the activity of an NADH-dependent cytochrome b5 reductase which is not incubated with a test compound.

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45 11. A method as claimed in claim 10, wherein, in step iii), the activity of the NADH-dependent cytochrome b5 reductase is determined by using iron(III) cytochrome b5, potassium

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iron(III)-cyanide, 2,6-dichlorophenolindophenol,  
methemerythrin, p-benzoquinone or  
5-hydroxy-1,4-naphthoquinone as the substrate.

- 5 12. A method as claimed in claim 9, which encompasses the  
following steps:
- 10 i. generating a transgenic organism as claimed in claim 7 or  
a transgenic organism comprising a nucleic acid sequence  
encoding a polypeptide with the biological activity of an  
NADH-dependent cytochrome b5 reductase consisting of
- 15 a) a nucleic acid sequence with the nucleic acid  
sequence shown in SEQ ID NO:1; or
- 20 b) a nucleic acid sequence which, on the basis of the  
degeneracy of the genetic code, can be deduced from  
the amino acid sequence shown in SEQ ID NO:2 by back  
translation; or
- 25 c) a functional equivalent of the nucleic acid sequence  
SEQ ID NO:1 with at least 52% identity with SEQ ID  
NO:1; or
- 30 d) a nucleic acid sequence which, on the basis of the  
degeneracy of the genetic code, can be deduced from  
the amino acid sequence of a functional equivalent of  
SEQ ID NO:2, which has at least 39% identity with SEQ  
ID NO:2, by back translation;
- 35 ii. applying a test substance to the transgenic organism of  
claim i) and to a nontransgenic organism of the same  
genotype;
- 40 iii. determining the growth or the viability of the transgenic  
and of the nontransgenic organisms after application of  
the test substance; and
- iv. selection of test substances which bring about a reduced  
growth or a reduced viability of the nontransgenic  
organism in comparison with the growth of the transgenic  
organism.
- 45 13. A method as claimed in claim 12, which is carried out in a  
plant organism or a yeast.

14. A method for identifying growth-regulatory compounds, comprising the following steps:
- 5 i. generation of a transgenic plant comprising a nucleic acid sequence encoding a polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase consisting of
    - 10 a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1; or
    - 15 b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translation; or
    - 20 c) a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 52% identity with SEQ ID NO:1; or
    - 25 d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence of a functional equivalent of SEQ ID NO:2, which has at least 39% identity with SEQ ID NO:2, by back translation; where the polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase is overexpressed in the transgenic plant;
  - 30 ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same variety;
  - 35 iii. determining the growth or the viability of the transgenic and of the nontransgenic plants after application of the test substance; and selection of test substances which bring about a modified growth of the nontransgenic plant in comparison with the growth of the transgenic plant.
15. A vehicle which has one or more of the nucleic acid molecules as claimed in any of claims 1 to 2, or one or more expression cassettes as claimed in claim 5, or one or more vectors as claimed in claim 6, or one or more organisms as claimed in claim 7 or one or more (poly)peptides as claimed in claim 3.
- 45 16. A method as claimed in any of claims 9 to 14, wherein the substances are identified in a high-throughput screening.

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17. A herbicidally active compound identified by one or the methods as claimed in any of claims 9 to 13 and 16.
18. A growth-regulatory compound identified by the method as  
5 claimed in claims 14 and 16.
19. A process for the preparation of an agrochemical composition, which comprises
- 10 a) identifying a herbicidally active compound by one or the methods as claimed in any of claims 9 to 13 and 16 or a growth-regulatory compound as claimed in claims 14 and 16; and
- 15 b) formulating this compound together with suitable auxiliaries to give herbicidally or growth-regulatory crop protection products.
20. A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one compound as claimed in claim 17 or 18 or a compound obtainable by the method stated in claim 19 to act on plants, their environment and/or on seeds.
- 25 21. The use of a compound as claimed in claim 17 or 18 or of an agrochemical formulation obtainable by the method stated in claim 19 in a method as claimed in claim 20 for controlling undesired vegetation and/or for regulating the growth of plants.
- 30 22. A method for generating nucleic acid sequences which
- 35 i) encode a polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase which is not inhibited by substances as claimed in claim 17; and which are comprised by a functional equivalent of the nucleic acid sequence of the nucleic acid sequence SEQ ID NO:1 with at least 52% identity with SEQ ID NO:1;
- 40 which comprises the following process steps:
- a) expression, in a heterologous system or in a cell-free system, of the proteins encoded by the nucleic acid according to i);
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- b) randomized or site-directed mutagenesis of the protein by modification of the nucleic acid;
  - c) measuring the interaction of the modified gene product with the herbicide;
  - d) identification of derivatives of the protein which show less interaction;
  - e) assaying the biological activity of the protein after application of the herbicide; and
  - f) selection of the nucleic acid sequences which show a modified biological activity toward the herbicide.
23. A method as claimed in claim 22, wherein the sequences selected in accordance with claim 22 f) are introduced into an organism.
24. A method for generating transgenic plants which are resistant to substances as claimed in claim 17, which comprises overexpressing, in these plants, a nucleic acid sequence encoding a polypeptide with the biological activity of an NADH-dependent cytochrome b5 reductase which comprises
- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1; or
  - b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by backtranslation; or
  - c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be deduced from the amino acid sequence of a functional equivalent of SEQ ID NO:2 which has at least 39% identity with SEQ ID NO:2; or
  - d) a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 52% identity with SEQ ID NO:1.
25. A transgenic plant, generated by a method as claimed in claim 24.